Exhibit C
Blast of SEQ ID NO: 1 versus human genome

MEGABLAST 1.2.3-Paracel [2001-11-20]

Reference:
Zheng Zhang, Scott Schwartz, Lukas Wagner, and Webb Miller (2000),
"A greedy algorithm for aligning DNA sequences",
J Comput Biol 2000; 7(1-2):203-14.
Database: Homo_sapiens.latestgp.masked.fa
            33,840 sequences; 200,810,911,373 total letters

Query= LEX121seqid1
          (747 letters)

Sequences producing significant alignments:	Score (bits)	E Value
AC135034.1.27032.29361	287	5e-75
AC025418.23.1.83000	287	5e-75
AC135034.1.59399.65233	174	5e-41

>AC135034.1.27032.29361
          Length = 2330

  Score = 287 bits (145), Expect = 5e-75
  Identities = 145/145 (100%)
  Strand = Plus / Plus


```
Query: 451   ttacagtgttgtggccaacataattacacagactggataaagaataagaacaaagaaaat 510
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1180  ttacagtgttgtggccaacataattacacagactggataaagaataagaacaaagaaaat 1239


Query: 511   tcaggacaggtgccatgttcttgcacaaagtcaactttaagaaaatggttttgtgatgag 570
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1240  tcaggacaggtgccatgttcttgcacaaagtcaactttaagaaaatggttttgtgatgag 1299


Query: 571   ccactgaatgcaacttaccttgagg 595
             |||||||||||||||||||||||||
Sbjct: 1300  ccactgaatgcaacttaccttgagg 1324
```


>AC025418.23.1.83000
          Length = 83000

  Score = 287 bits (145), Expect = 5e-75
  Identities = 145/145 (100%)
  Strand = Plus / Minus


```
Query: 451   ttacagtgttgtggccaacataattacacagactggataaagaataagaacaaagaaaat 510
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 48068 ttacagtgttgtggccaacataattacacagactggataaagaataagaacaaagaaaat 48009
```

```
Query: 511   tcaggacaggtgccatgttcttgcacaaagtcaactttaagaaaatggttttgtgatgag 570
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 48008 tcaggacaggtgccatgttcttgcacaaagtcaactttaagaaaatggttttgtgatgag 47949


Query: 571   ccactgaatgcaacttaccttgagg 595
             |||||||||||||||||||||||||
Sbjct: 47948 ccactgaatgcaacttaccttgagg 47924



 Score =  250 bits (126), Expect = 1e-63
 Identities = 126/126 (100%)
 Strand = Plus / Minus


Query: 139   gatgaaaataatcacttcatagtacctatttctcaaattttgattggaatgggatcttct 198
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 58492 gatgaaaataatcacttcatagtacctatttctcaaattttgattggaatgggatcttct 58433


Query: 199   actgttcttttttgtctattgggttatataggaattcacaacgaaatcagatggctccta 258
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 58432 actgttcttttttgtctattgggttatataggaattcacaacgaaatcagatggctccta 58373


Query: 259   attgtg 264
             ||||||
Sbjct: 58372 attgtg 58367



 Score =  224 bits (113), Expect = 6e-56
 Identities = 113/113 (100%)
 Strand = Plus / Minus


Query: 338   aggttcagcaactatggcatgacaaaattgattttgtcatttctgagtatggatctaaag 397
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 50207 aggttcagcaactatggcatgacaaaattgattttgtcatttctgagtatggatctaaag 50148


Query: 398   ataagcctgaagatataaccaagtggactattctgaatgccttacagaaaaca 450
             |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 50147 ataagcctgaagatataaccaagtggactattctgaatgccttacagaaaaca 50095



 Score =  174 bits (88), Expect = 5e-41
 Identities = 88/88 (100%)
 Strand = Plus / Minus


Query: 593   agggttgtgaaaataaaatcagtgcatggtataatgttaatgtgttaaccttaatcggaa 652
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 46442 agggttgtgaaaataaaatcagtgcatggtataatgttaatgtgttaaccttaatcggaa 46383


Query: 653   ttaactttggactttttaacttcagaggt 680
             |||||||||||||||||||||||||||||
```

```
Sbjct: 46382 ttaactttggactttttaacttcagaggt 46355
```

```
 Score =  155 bits (78), Expect = 5e-35
 Identities = 78/78 (100%)
 Strand = Plus / Minus
```

```
Query: 264    gtatgcagtattgataacatggacctttgctgttcaggttgtactttcagcattcatcat 323
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 53869 gtatgcagtattgataacatggacctttgctgttcaggttgtactttcagcattcatcat 53810
```

```
Query: 324    cacaaagaaagaggaggt 341
              ||||||||||||||||||
Sbjct: 53809 cacaaagaaagaggaggt 53792
```

```
 Score =  147 bits (74), Expect = 1e-32
 Identities = 74/74 (100%)
 Strand = Plus / Minus
```

```
Query: 66     ggttcttggactttttattcatgggatttggtgcatggctcttattagatagaaataattt 125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 60260 ggttcttggactttttattcatgggatttggtgcatggctcttattagatagaaataattt 60201
```

```
Query: 126    tttaacagcttttg 139
              ||||||||||||||
Sbjct: 60200 tttaacagcttttg 60187
```

```
 Score =  141 bits (71), Expect = 7e-31
 Identities = 71/71 (100%)
 Strand = Plus / Minus
```

```
Query: 677    aggttttccaagtctcattaacagtttgtttcttcaaaaacatcaagaatataatccatg 736
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 45026 aggttttccaagtctcattaacagtttgtttcttcaaaaacatcaagaatataatccatg 44967
```

```
Query: 737    cagaaatgtga 747
              |||||||||||
Sbjct: 44966 cagaaatgtga 44956
```

```
 Score =  135 bits (68), Expect = 4e-29
 Identities = 68/68 (100%)
 Strand = Plus / Minus
```

```
Query: 1      atgttaagaaataacaaaacaataattattaagtactttcttaatctcattaatggagct 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 60414 atgttaagaaataacaaaacaataattattaagtactttcttaatctcattaatggagct 60355
```

```
Query: 61      ttcttggt 68
               || ||||||
Sbjct: 60354 ttcttggt 60347


>AC135034.1.59399.65233
          Length = 5835

 Score =  174 bits (88), Expect = 5e-41
 Identities = 88/88 (100%)
 Strand = Plus / Minus


Query: 593   agggttgtgaaaataaaatcagtgcatggtataatgttaatgtgttaaccttaatcggaa 652
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 5352  agggttgtgaaaataaaatcagtgcatggtataatgttaatgtgttaaccttaatcggaa 5293


Query: 653   ttaactttggactttttaacttcagaggt 680
             |||||||||||||||||||||||||||||
Sbjct: 5292  ttaactttggactttttaacttcagaggt 5265



 Score =  141 bits (71), Expect = 7e-31
 Identities = 71/71 (100%)
 Strand = Plus / Minus


Query: 677   aggttttccaagtctcattaacagtttgtttcttcaaaaacatcaagaatataatccatg 736
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 3942  aggttttccaagtctcattaacagtttgtttcttcaaaaacatcaagaatataatccatg 3883


Query: 737   cagaaatgtga 747
             |||||||||||
Sbjct: 3882  cagaaatgtga 3872
```